

6P/1648
PATENT
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Case Docket No. NADII.022A
Date: October 2, 2002

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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

TECH CENTER 1600/2900

Applicant(s) : Haynes, et al.
Appl. No. : 10/057,789
Filed : January 25, 2002
For : DIFFERENTIAL LABELING
FOR QUANTITATIVE
ANALYSIS OF COMPLEX
PROTEIN MIXTURES
Examiner : Unknown
Group Art Unit : 1648

I hereby certify that this correspondence and all marked
attachments are being deposited with the United States
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October 2, 2002

(Date)

Sam K. Tahmassebi, Reg. No. 45,151

TRANSMITTAL LETTER

United States Patent and Trademark Office
P.O. Box 2327
Arlington, VA 22202

ATTENTION: APPLICATION BRANCH

Dear Sir:

Enclosed for filing in the above-identified application are:

(X) An Information Disclosure Statement.

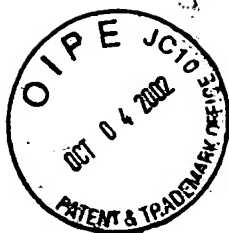
(X) A PTO Form 1449 with twenty-three (23) references.

(X) The Commissioner is hereby authorized to charge any additional fees which may be required, or
credit any overpayment, to Account No. 11-1410.

(X) Return prepaid postcard.

Sam K. Tahmassebi
Registration No. 45,151
Attorney of Record

NADIL022A



PATENT

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INFORMATION DISCLOSURE STATEMENT

United States Patent and Trademark Office
P.O. Box 2327
Arlington, VA 22202

Dear Sir:

Enclosed is form PTO-1449 listing references that are also enclosed. This Information Disclosure Statement is being filed before the receipt of a first Office Action on the merits, and presumably no fee is required in accordance with 37 C.F.R. § 1.97(b)(3). If a first Office Action on the merits was mailed before the mailing date of this Statement, the Commissioner is authorized to charge the fee set forth in 37 C.F.R. § 1.17(p) to Deposit Account No. 11-1410.

Respectfully submitted,

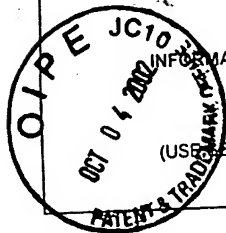
KNOBBE, MARTENS, OLSON & BEAR, LLP

Dated: Oct. 2, 2002

By: Sam K. Tahmassebi
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Registration No. 45,151
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FORM PTO-1449 U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE		ATTY. DOCKET NO. NADII.022A	APPLICATION NO. 10/057,789
INFORMATION DISCLOSURE STATEMENT BY APPLICANT (USE SEVERAL SHEETS IF NECESSARY)		APPLICANT Haynes et al.	
		FILING DATE January 25, 2002	GROUP 1648

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U.S. PATENT DOCUMENTS						
EXAMINER INITIAL		DOCUMENT NUMBER	DATE	NAME	CLASS	SUBCLASS
	1	5,538,897	07/23/96	Yates		

EXAMINER INITIAL	OTHER DOCUMENTS (INCLUDING AUTHOR, TITLE, DATE, PERTINENT PAGES, ETC.)	
	2	Boucherie <i>et al.</i> , Two-dimensional gel protein database of <i>Saccharomyces cerevisiae</i> , <i>Electrophoresis</i> 17:1683-1699 (1996)
	3	Dongr'e <i>et al.</i> , Emerging tandem-mass-spectrometry techniques for the rapid identification of proteins, <i>Trends Biotechnol</i> 15:418-425 (1997)
	4	Ducet <i>et al.</i> , High throughput protein characterization by automated reverse-phase chromatography/electrospray tandem mass spectrometry, <i>Prot Sci</i> 7:706-719 (1998)
	5	Eng <i>et al.</i> , An approach to correlate tandem mass spectral data of peptides with amino acid sequences in a protein database, <i>J Am Soc Mass Spectrom</i> 5:976-980 (1994)
	6	Figeys and Aebersold, High sensitivity analysis of proteins and peptides by capillary electrophoresis-tandem mass spectrometry: Recent developments in technology and applications, <i>Electrophoresis</i> 19:885-892 (1998)
	7	Figeys <i>et al.</i> , A microfabricated device for rapid protein identification by microelectrospray ion trap mass spectrometry, <i>Anal Chem</i> 69:3153-3160 (1997)
	8	Figeys <i>et al.</i> , Protein identification by solid phase microextraction—capillary zone electrophoresis—microelectrospray—tandem mass spectrometry, <i>Nature Biotech</i> 14:1579-1583 (1996)
	9	Garrels <i>et al.</i> , Proteome studies of <i>Saccharomyces cerevisiae</i> : Identification and characterization of abundant proteins, <i>Electrophoresis</i> 18:1347-1360 (1997)
	10	Gygi <i>et al.</i> , Quantitative analysis of complex protein mixtures using isotope-coded affinity tags, <i>Nature Biotechnol</i> 17:994-999 (1999)
	11	Gygi <i>et al.</i> , Correlation between protein and mRNA abundance in yeast, <i>Cell Biol</i> 19:1720-1730 (1999)
	12	Gygi <i>et al.</i> , Protein analysis by mass spectrometry and sequence database searching: Tools for cancer research in the post-genomic era, <i>Electrophoresis</i> 20:310-319 (1999)
	13	Haynes <i>et al.</i> , Identification of gel-separated proteins by liquid chromatography-electrospray tandem mass spectrometry: Comparison of methods and their limitations, <i>Electrophoresis</i> 19:939-945 (1998)
	14	Link <i>et al.</i> , Identifying the major proteome components of <i>Haemophilus influenzae</i> type-strain NCTC 8143, <i>Electrophoresis</i> 18:1314-1334 (1997)
	15	Link <i>et al.</i> , Direct analysis of protein complexes using mass spectrometry, <i>Nat Biotech</i> , 17:676-682 (1999)
	16	Mann and Wilm, Error-tolerant identification of peptides in sequence databases by peptide sequence tags, <i>Anal Chem</i> 66:4390-4399 (1994)

EXAMINER	DATE CONSIDERED
*EXAMINER: INITIAL IF CITATION CONSIDERED. WHETHER OR NOT CITATION IS IN CONFORMANCE WITH MPEP 609: DRAW LINE THROUGH CITATION IF NOT IN CONFORMANCE AND NOT CONSIDERED. INCLUDE COPY OF THIS FORM WITH NEXT COMMUNICATION TO APPLICANT.	

FORM PTO-1449

U.S. DEPARTMENT OF COMMERCE
PATENT AND TRADEMARK OFFICEATTY. DOCKET NO.
NADII.022AAPPLICATION NO
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EXAMINER INITIAL	OTHER DOCUMENTS (INCLUDING AUTHOR, TITLE, DATE, PERTINENT PAGES, ETC.)
17	Opitek <i>et al.</i> , Comprehensive on-line LC/LC/MS of proteins, <i>Anal Chem</i> 69:1518-1524 (1997)
18	Pennington <i>et al.</i> , Proteome analysis: from protein characterization to biological function, <i>Trends Cell Bio</i> 7:168-173 (1997)
19	Shalon <i>et al.</i> , A DNA microarray system for analyzing complex DNA samples using two-color fluorescent probe hybridization, <i>Genome Res</i> 6:639-645 (1996)
20	Shevchenko <i>et al.</i> , Mass spectrometric sequencing of proteins from silver-stained polyacrylamide gels, <i>Anal Chem</i> 68:850-858 (1996)
21	Shevchenko <i>et al.</i> , Linking genome and proteome by mass spectrometry: large-scale identification of yeast proteins from two dimensional gels, <i>Proc Natl Acad Sci USA</i> 93:14440-14445 (1996)
22	Velculescu <i>et al.</i> , Characterization of the Yeast Transcriptome, <i>Cell</i> 88:243-251 (1997)
23	Yates <i>et al.</i> , Method to correlate tandem mass spectra of modified peptides to amino acid sequences in the protein database, <i>Anal Chem</i> 67:1426-1436 (1995)

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